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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/058,945

DATE: 02/19/2002
TIME: 11:02:15

Input Set : A:\215482US0X.txt
Output Set: N:\CRF3\02192002\J058945.raw

ENTERED

3 <110> APPLICANT: HERMANN, Thomas
 4 WOLF, Andreas
 5 MORBACH, Susanne
 6 KRAMER, Reinhard
 8 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE OtsA PROTEIN
 10 <130> FILE REFERENCE: 215482US0X
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/058,945
 C--> 12 <141> CURRENT FILING DATE: 2002-01-30
 12 <150> PRIOR APPLICATION NUMBER: DE 10103873.9
 13 <151> PRIOR FILING DATE: 2001-01-30
 15 <150> PRIOR APPLICATION NUMBER: DE 10110760.9
 16 <151> PRIOR FILING DATE: 2000-03-07
 18 <160> NUMBER OF SEQ ID NOS: 4
 20 <170> SOFTWARE: PatentIn version 3.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 3010
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Corynebacterium glutamicum
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (884)..(2338)
 30 <223> OTHER INFORMATION:
 33 <400> SEQUENCE: 1
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 36 ggccccgtct ctgcccgtgc gattgctgca acagcagttg gtttcactgg tggtttgctt 120
 38 gcccgtcgat tcttgattcc accgttgatt gtggcgattt ccggcatcac accaatgctt 180
 40 ccaggtcttag caatttaccg cggaaatgtac gccaccctga atgatcaaacc actcatgggt 240
 42 ttccaccaaca ttgcgggttgc tttagccact gtttcatcac ttgccgctgg cgtgggtttt 300
 44 ggtgagtggaa ttgcccgcag gctacgtcgt ccaccacgct tcaaccata ccgtgcattt 360
 46 accaaggcga atgagtctc ctccaggag gaagctgagc agaatcagcg cggcagaga 420
 48 aaacgtccaa agactaatca gagattcggt aataaaaaggta aaaaatcaac ctgcttaggc 480
 50 gtcttgcgt taaatagcgt agaataatcgg gtcgatcgct tttaaacact caggaggatc 540
 52 ctgccggcc aaaatcacgg acactcgcc caccccgaaa tcccttcacg ctgttgaaga 600
 54 ggaaaccgca gccgggtcccc gcaggattgt tgccacctat tctaaggact tcttcgacgg 660
 56 cgtcaacttgc atgtgcattgc tcggcggtga acctcaggac ctgcgttaca ccaagggtcgc 720
 58 ttctgaacac gaggaagctc agccaaagaa ggctacaaag cggactcgta aggcaccacg 780
 60 taagaaggct gctgctaaga aaacgaccaa gaagaccact aaaaaacta ctaaaaagac 840
 62 caccgcaaaag aagaccacaa agaagtctt agccggatct tat atg gat gat tcc 895
 63 Met Asp Asp Ser
 64 1
 66 aat agc ttt gta gtt gtt gct aac cgt ctg cca gtg gat atg act gtc 943
 67 Asn Ser Phe Val Val Val Ala Asn Arg Leu Pro Val Asp Met Thr Val
 68 5 10 15 20

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70	cac cca gat ggt agc tat agc atc tcc ccc agc ccc ggt ggc ctt gtc	991
71	His Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro Gly Gly Leu Val	
72	25 30 35	
74	acg ggg ctt tcc ccc gtt ctg gaa caa cat cgt gga tgt tgg gtc gga	1039
75	Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly Cys Trp Val Gly	
76	40 45 50	
78	tgg cct gga act gta gat gtt gca ccc gaa cca ttt cga aca gat acg	1087
79	Trp Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe Arg Thr Asp Thr	
80	55 60 65	
82	ggt gtt ttg ctg cac cct gtt gtc ctc act gca agt gac tat gaa ggc	1135
83	Gly Val Leu Leu His Pro Val Val Leu Thr Ala Ser Asp Tyr Glu Gly	
84	70 75 80	
86	ttc tac gag ggc ttt tca aac gca acg ctg tgg cct ctt ttc cac gat	1183
87	Phe Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro Leu Phe His Asp	
88	85 90 95 100	
90	ctg att gtt act ccg gtg tac aac acc gat tgg tgg cat gcg ttt cg	1231
91	Leu Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp His Ala Phe Arg	
92	105 110 115	
94	gag gta aac ctc aag ttc gct gaa gcc gtg agc caa gtg gcg gca cac	1279
95	Glu Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln Val Ala Ala His	
96	120 125 130	
98	ggt gcc act gtg tgg gtg cag gac tat cag ctg tgg ctg gtt cct ggc	1327
99	Gly Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu Val Pro Gly	
100	135 140 145	
102	att ttg cgc cag atg cgc cct gat ttg aag atc ggt ttc ttc ctc cac	1375
103	Ile Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly Phe Phe Leu His	
104	150 155 160	
106	att ccc ttc cct tcc cct gat ctg ttc cgt cag ctg ccg tgg cgt gaa	1423
107	Ile Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu Pro Trp Arg Glu	
108	165 170 175 180	
110	gag att gtt cga ggc atg ctg ggc gca gat ttg gtg gga ttc cat ttg	1471
111	Glu Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val Gly Phe His Leu	
112	185 190 195	
114	gtt caa aac gca gaa aac ttc ctt gcg tta acc acc cag cag gtt gcc ggc	1519
115	Val Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln Gln Val Ala Gly	
116	200 205 210	
118	act gcc ggg tct cat gtg ggt cag ccg gac acc ttg cag gtc agt ggt	1567
119	Thr Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu Gln Val Ser Gly	
120	215 220 225	
122	gaa gca ttg gtg cgt gag att ggc gct cat gtt gaa acc acc gct gac gga	1615
123	Glu Ala Leu Val Arg Glu Ile Gly Ala His Val Glu Thr Ala Asp Gly	
124	230 235 240	
126	agg cga gtt agc gtc ggg gcg ttc ccg atc tcg att gat gtt gaa atg	1663
127	Arg Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile Asp Val Glu Met	
128	245 250 255 260	
130	ttt ggg gag gcg tcg aaa agc gcc gtt ctt gat ctt tta aaa acg ctc	1711
131	Phe Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu Leu Lys Thr Leu	
132	265 270 275	
134	gac gag ccg gaa acc gta ttc ctg ggc gtt gac cga ctg gac tac acc	1759

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135	Asp Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg Leu Asp Tyr Thr			
136	280	285	290	
138	aag ggc att ttg cag cgc ctg ctt gcg ttt gag gaa ctg ctg gaa tcc		1807	
139	Lys Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu Leu Leu Glu Ser			
140	295	300	305	
142	ggc gcg ttg gag gcc gac aaa gct gtg ttg ctg cag gtc gcg acg cct		1855	
143	Gly Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln Val Ala Thr Pro			
144	310	315	320	
146	tcg cgt gag cgc att gat cac tat cgt gtg tcg cgt tcg cag gtc gag		1903	
147	Ser Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg Ser Gln Val Glu			
148	325	330	335	340
150	gaa gcc gtc ggc cgt atc aat ggt cgt ttc ggt cgc atg ggg cgt ccc		1951	
151	Glu Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg Met Gly Arg Pro			
152	345	350	355	
154	gtg gtg cat tat cta cac agg tca ttg agc aaa aat gat ctc cag gtg		1999	
155	Val Val His Tyr Leu His Arg Ser Leu Ser Lys Asn Asp Leu Gln Val			
156	360	365	370	
158	ctg tat acc gca gcc gat gtc atg ctg gtt acg cct ttt aaa gac ggt		2047	
159	Leu Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro Phe Lys Asp Gly			
160	375	380	385	
162	atg aac ttg gtg gct aaa gaa ttc gtg gcc aac cac cgc gac ggc act		2095	
163	Met Asn Leu Val Ala Lys Glu Phe Val Ala Asn His Arg Asp Gly Thr			
164	390	395	400	
166	ggt gct ttg gtg ctg tcc gaa ttt gcc ggc gcg gcc act gag ctg acc		2143	
167	Gly Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala Thr Glu Leu Thr			
168	405	410	415	420
170	ggt gcg tat tta tgc aac cca ttt gat gtg gaa tcc atc aaa cgg caa		2191	
171	Gly Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser Ile Lys Arg Gln			
172	425	430	435	
174	atg gtg gca gct gtc cat gat ttg aag cac aat ccg gaa tct gcg gca		2239	
175	Met Val Ala Ala Val His Asp Leu Lys His Asn Pro Glu Ser Ala Ala			
176	440	445	450	
178	acg cga atg aaa acg aac agc gag cag gtc tat acc cac gac gtc aac		2287	
179	Thr Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr His Asp Val Asn			
180	455	460	465	
182	gtg tgg gct aat agt ttc ctg gat tgt ttg gca cag tcg gga gaa aac		2335	
183	Val Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln Ser Gly Glu Asn			
184	470	475	480	
186	tca tgaaccgcgc acgaatcgcg accataggcg ttctccgct tgctttactg		2388	
187	Ser			
188	485			
190	ctggcgtcct gtggtcaga caccgtggaa atgacagatt ccacctgggt ggtgaccaat		2448	
192	attcacccg atccagatga gtcgaattcg atcagtaatc ttgtcatttc ccagccccagc		2508	
194	ttagattttg gcaattcttc cctgtctgg ttcactggct gtgtgccttt tacggggcgt		2568	
196	gccaattct tccaaaatgg tgagcaaagc tctgttctgg atgccgatata tgtgacccat		2628	
198	tcttccctgg atttcgataa acttcccgt gattgccaag gacaagaact caaatttcat		2688	
200	aacgagctgg ttgatcttct gcctgggtt tttgaaatct ccaggacttc tggttcagaa		2748	
202	atcttgctga cttagcgtgt cgatgaactc gatggccag caatccgctt ggtgtcctgg		2808	
204	atcgccgca catctaagg tgccagggtt ttaaaagtgcc aggggttctg tgggatccgt		2868	

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206 acactggttc ccatgactt gactatttag gaaatcgcca agacaaaaa gctttgggtt 2928
 208 gtgtccgatt ttgatggAAC catgcagGA tttAGCAAGG acgCTTACAA cgTTCCATC 2988
 210 aaccagaaat ccctcaaggc gg 3010
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 215 <212> TYPE: PRT
 216 <213> ORGANISM: Corynebacterium glutamicum
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 220 Met Asp Asp Ser Asn Ser Phe Val Val Val Ala Asn Arg Leu Pro Val
 221 1 5 10 15
 224 Asp Met Thr Val His Pro Asp Gly Ser Tyr Ser Ile Ser Pro Ser Pro
 225 20 25 30
 228 Gly Gly Leu Val Thr Gly Leu Ser Pro Val Leu Glu Gln His Arg Gly
 229 35 40 45
 232 Cys Trp Val Gly Trp Pro Gly Thr Val Asp Val Ala Pro Glu Pro Phe
 233 50 55 60
 236 Arg Thr Asp Thr Gly Val Leu Leu His Pro Val Val Leu Thr Ala Ser
 237 65 70 75 80
 240 Asp Tyr Glu Gly Phe Tyr Glu Gly Phe Ser Asn Ala Thr Leu Trp Pro
 241 85 90 95
 244 Leu Phe His Asp Leu Ile Val Thr Pro Val Tyr Asn Thr Asp Trp Trp
 245 100 105 110
 248 His Ala Phe Arg Glu Val Asn Leu Lys Phe Ala Glu Ala Val Ser Gln
 249 115 120 125
 252 Val Ala Ala His Gly Ala Thr Val Trp Val Gln Asp Tyr Gln Leu Leu
 253 130 135 140
 256 Leu Val Pro Gly Ile Leu Arg Gln Met Arg Pro Asp Leu Lys Ile Gly
 257 145 150 155 160
 260 Phe Phe Leu His Ile Pro Phe Pro Ser Pro Asp Leu Phe Arg Gln Leu
 261 165 170 175
 264 Pro Trp Arg Glu Glu Ile Val Arg Gly Met Leu Gly Ala Asp Leu Val
 265 180 185 190
 268 Gly Phe His Leu Val Gln Asn Ala Glu Asn Phe Leu Ala Leu Thr Gln
 269 195 200 205
 272 Gln Val Ala Gly Thr Ala Gly Ser His Val Gly Gln Pro Asp Thr Leu
 273 210 215 220
 276 Gln Val Ser Gly Glu Ala Leu Val Arg Glu Ile Gly Ala His Val Glu
 277 225 230 235 240
 280 Thr Ala Asp Gly Arg Arg Val Ser Val Gly Ala Phe Pro Ile Ser Ile
 281 245 250 255
 284 Asp Val Glu Met Phe Gly Glu Ala Ser Lys Ser Ala Val Leu Asp Leu
 285 260 265 270
 288 Leu Lys Thr Leu Asp Glu Pro Glu Thr Val Phe Leu Gly Val Asp Arg
 289 275 280 285
 292 Leu Asp Tyr Thr Lys Gly Ile Leu Gln Arg Leu Leu Ala Phe Glu Glu
 293 290 295 300
 296 Leu Leu Glu Ser Gly Ala Leu Glu Ala Asp Lys Ala Val Leu Leu Gln
 297 305 310 315 320
 300 Val Ala Thr Pro Ser Arg Glu Arg Ile Asp His Tyr Arg Val Ser Arg

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301 325 330 335
304 Ser Gln Val Glu Glu Ala Val Gly Arg Ile Asn Gly Arg Phe Gly Arg
305 340 345 350
308 Met Gly Arg Pro Val Val His Tyr Leu His Arg Ser Leu Ser Lys Asn
309 355 360 365
312 Asp Leu Gln Val Leu Tyr Thr Ala Ala Asp Val Met Leu Val Thr Pro
313 370 375 380
316 Phe Lys Asp Gly Met Asn Leu Val Ala Lys Glu Phe Val Ala Asn His
317 385 390 395 400
320 Arg Asp Gly Thr Gly Ala Leu Val Leu Ser Glu Phe Ala Gly Ala Ala
321 405 410 415
324 Thr Glu Leu Thr Gly Ala Tyr Leu Cys Asn Pro Phe Asp Val Glu Ser
325 420 425 430
328 Ile Lys Arg Gln Met Val Ala Ala Val His Asp Leu Lys His Asn Pro
329 435 440 445
332 Glu Ser Ala Ala Thr Arg Met Lys Thr Asn Ser Glu Gln Val Tyr Thr
333 450 455 460
336 His Asp Val Asn Val Trp Ala Asn Ser Phe Leu Asp Cys Leu Ala Gln
337 465 470 475 480
340 Ser Gly Glu Asn Ser
341 485
344 <210> SEQ ID NO: 3
345 <211> LENGTH: 24
346 <212> TYPE: DNA
347 <213> ORGANISM: Corynebacterium glutamicum
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350 cacctattct aaggacttct tcga 24
353 <210> SEQ ID NO: 4
354 <211> LENGTH: 22
355 <212> TYPE: DNA
356 <213> ORGANISM: Corynebacterium glutamicum
358 <400> SEQUENCE: 4
359 accaaccagg tggaatctgt ca 22

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date